

**Inhibitory effect and mechanism of *Tagetes erecta* L. fungicide on *Fusarium oxysporum* f. sp.
*niveum***

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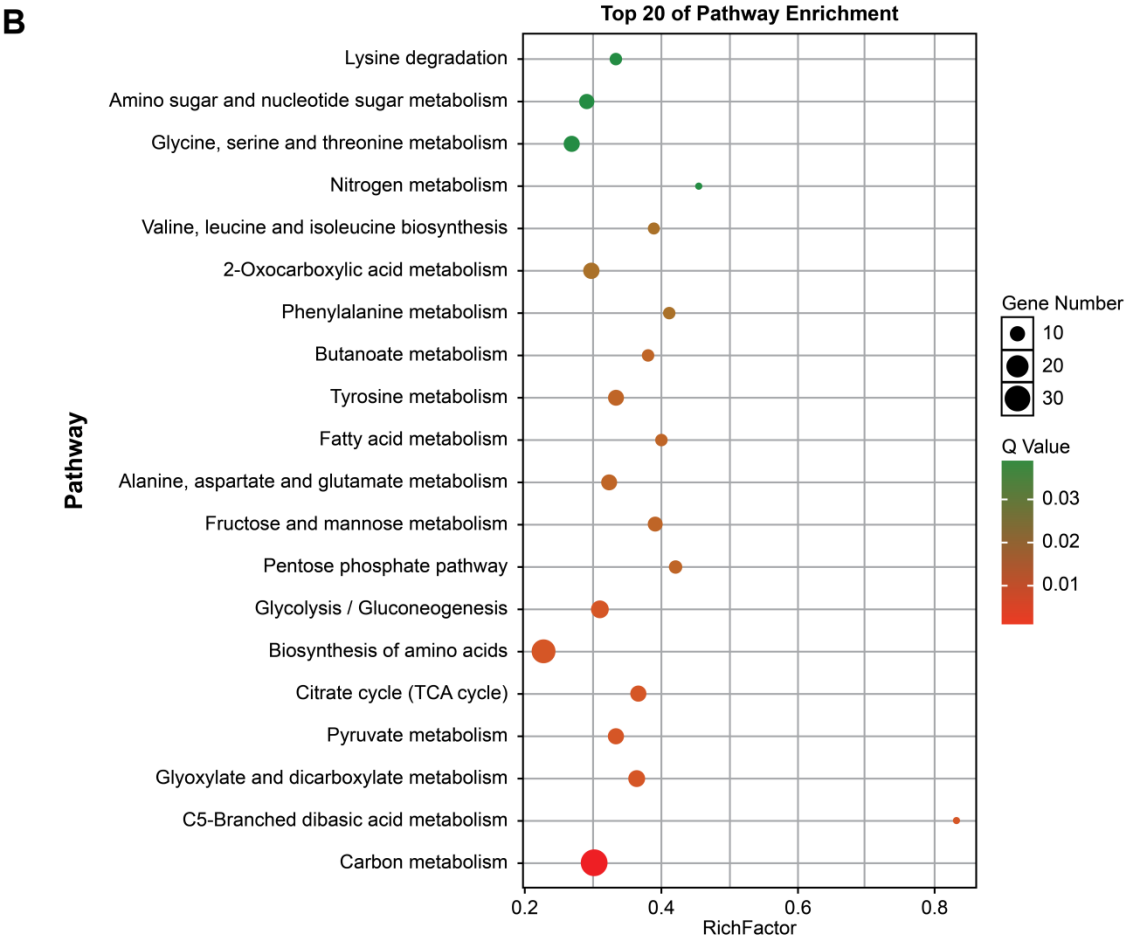
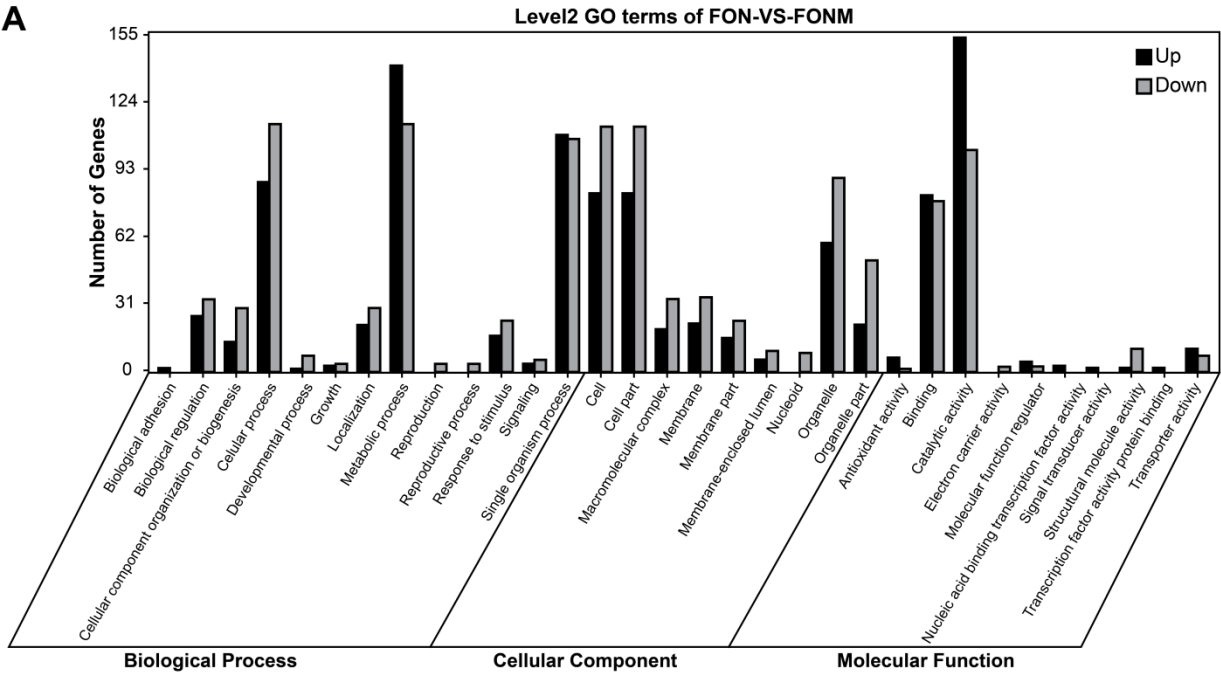
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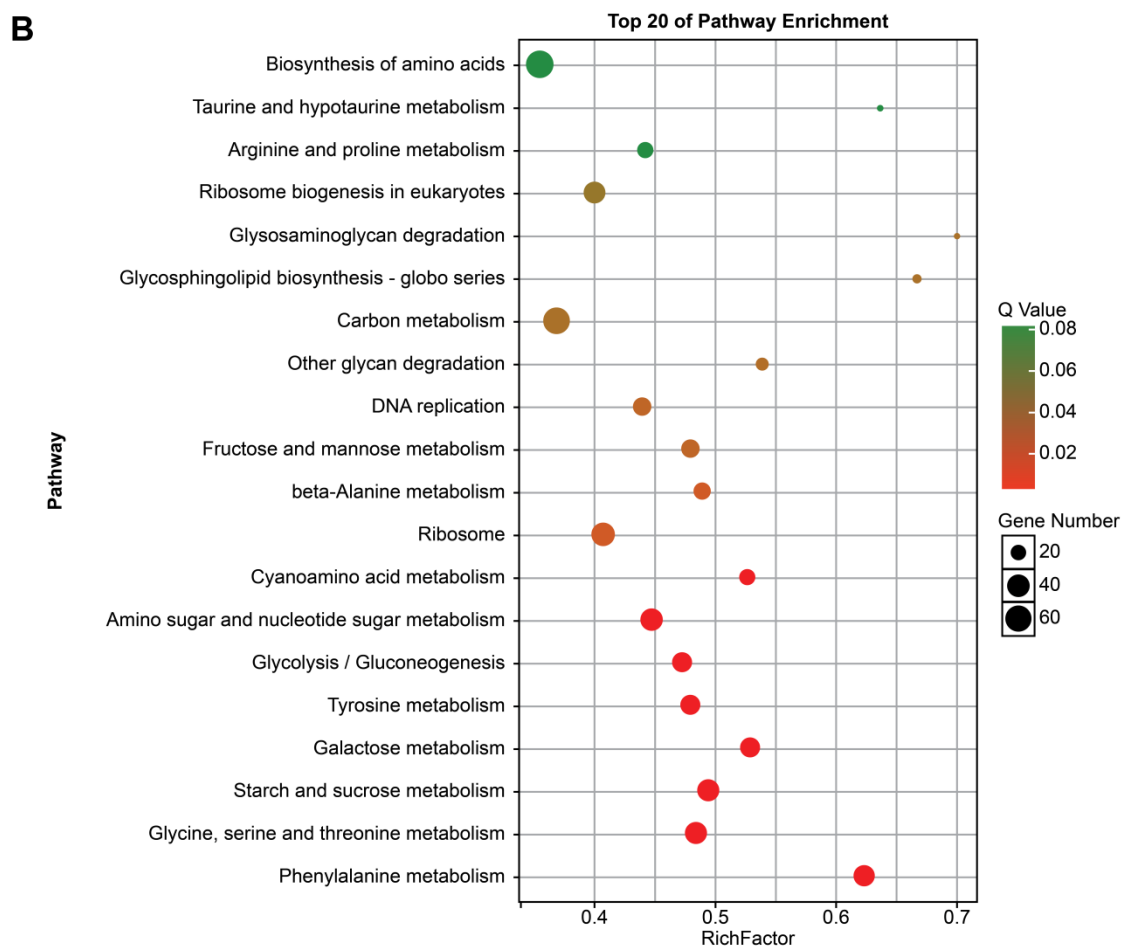
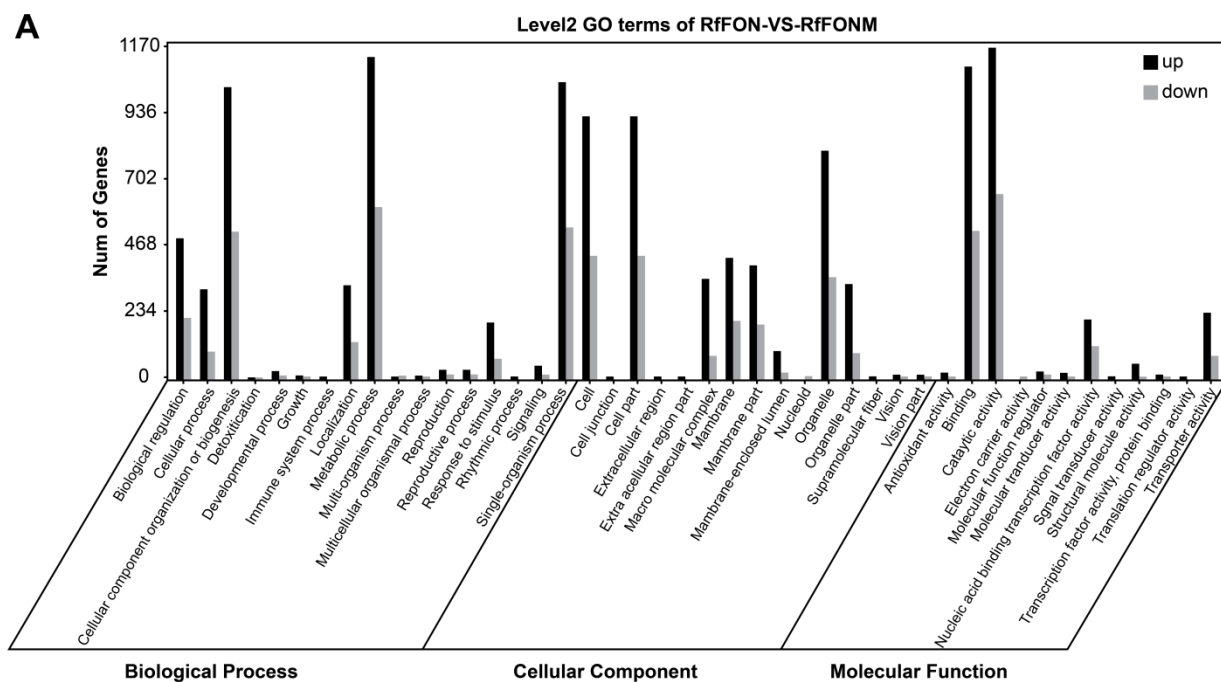
1 SUPPLEMENTARY FIGURES



2

3 Supplementary Fig S1. GO and KEGG analysis for differentially expressed proteins

- 1 A) GO analysis
- 2 B) KEGG analysis
- 3
- 4



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2 Supplementary Fig S2. GO and KEGG analysis of differentially expressed genes

3 A) GO analysis

1 B) KEGG analysis

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1 **SUPPLEMENTARY TABLES**

2 Supplementary Table S1. Summary of iTRAQ results

Content	Number
Unique Spectra/ Spectra/Total Spectra	86157/86963/409529
Unique Peptides/Peptides	18915/19047
Proteins	3238

3

1 Supplementary Table S2. Summary of transcriptional sequencing and assembly

Database	FON	FONM
Total clean reads	132806124	108518476
Total length of clean reads (bp)	13240999690	10824084784
Q20 (%)	98.00	98.03
GC (%)	56.10	55.78
Assembly	Trinity	
Number of unigenes	20889	
Total length of unigenes (bp)	21725882	
Average unigene length (bp)	1040	
Maximum unigene length (bp)	8778	
Minimum unigene length (bp)	201	
N50 (bp)	1800	

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1 Supplementary Table S3. The five most significant differences in protein and mRNA expression
2 from quadrants 3 and 7

Protein Acc.	FC	Description	Organism Species	Function
10 proteins in quadrant 3				
KPA45161.1	2.17	Methyltransferase protein	<i>Fusarium langsethiae</i>	Transferase activity
ENH63236.1	2.11	Autolysin	<i>Fusarium oxysporum</i>	-
XP_0025618 61.1	1.98	Pc18g00140	<i>Penicillium rubens</i>	Hydrolase activity
KPA45980.1	1.86	Leucine aminopeptidase 2	<i>Fusarium langsethiae</i>	Hydrolase and exopeptidase activity
ENH70301.1	1.81	6-hydroxy-D-nicotine oxidase	<i>Fusarium oxysporum</i>	Organic cyclic compound binding
KPA37072.1	1.72	Carboxypeptidase a4	<i>Fusarium langsethiae</i>	Metal ion binding; hydrolase activity
KPA39795.1	1.66	Membrane primary amine oxidase	<i>Fusarium langsethiae</i>	Metal ion binding; oxidoreductase activity
EWZ32741.1	1.58	Glycerol kinase	<i>Fusarium oxysporum</i>	Catalytic, kinase and transferase activity
CCT67575.1	1.49	Probable DUF895 domain Membrane protein	<i>Fusarium fujikuroi</i>	Intrinsic component of membrane
KPA38465.1	1.46	Aliphatic nitrilase	<i>Fusarium</i>	Hydrolase activity

langsethiae

10 RNA in quadrant 3				
KIL86238.1	9.52	Multidrug resistance protein	<i>Fusarium avenaceum</i>	Intrinsic component of membrane; Active transmembrane transporter activity
KPA38368.1	8.67	FAD containing protein	<i>Fusarium langsethiae</i>	Organic cyclic compound binding
XP_002561861.1	8.36	Pc18g00140	<i>Penicillium rubens</i>	Organic cyclic compound catabolic
EXK76462.1	8.30	Hypothetical protein FOQG_18796	<i>Fusarium oxysporum</i>	-
EXK76461.1	8.28	Hypothetical protein FOQG_18795	<i>Fusarium oxysporum</i>	-
ENH70301.1	7.52	6-hydroxy-D-nicotine oxidase	<i>Fusarium oxysporum</i>	Organic cyclic compound binding
KPA42579.1	6.50	rRNA 2-o-methyltransferase	<i>Fusarium langsethiae</i>	Intracellular organelle part
KPA38368.1	6.35	FAD containing protein	<i>Fusarium langsethiae</i>	Heterocyclic compound binding;
XP_011320935.1	6.24	Amino-acid permease inda1	<i>Fusarium graminearum</i>	Intrinsic component of membrane; Anion transmembrane transporter activity
EWG53161.1	5.94	Endoribonuclease L-PSP	<i>Fusarium verticillioides</i>	Catalytic activity
10 proteins in quadrant 7				

KPA38919.1	-1.92	22kda glycoprotein	<i>Fusarium langsethiae</i>	-
CCT63608.1	-1.73	Probable rAsp f 9 allergen	<i>Fusarium fujikuroi</i>	Hydrolase activity
KPA36188.1	-1.56	Small secreted protein	<i>Fusarium langsethiae</i>	-
KPA41277.1	-1.56	Nitric oxide dioxygenase	<i>Fusarium langsethiae</i>	Oxidoreductase activity
KPA41668.1	-1.56	Quinone oxidoreductase 2	<i>Fusarium langsethiae</i>	-
KIL85323.1	-1.05	Fumarylacetoacetase	<i>Fusarium avenaceum</i>	Hydrolase activity; acting on acid carbon-carbon bonds of ketonic substances
SCB64018.1	-0.93	Unnamed protein product	<i>Fusarium graminearum</i>	-
KPA45353.1	-0.89	Transcription factor	<i>Fusarium langsethiae</i>	-
KPA39782.1	-0.89	Phenolic acid decarboxylase PADC	<i>Fusarium langsethiae</i>	Carbon-carbon lyase activity
XP_009652260.1	-0.86	Allergen	<i>Verticillium dahliae</i>	-
10 RNA in 7 quadrant				
KPA45183.1	-10.11	Phosphoenolpyruvate carboxykinase	<i>Fusarium langsethiae</i>	Carboxy-lyase activity

CCT64874.1	-8.15	Related to <i>P. aeruginosa</i> hyuA and hyuB	<i>Fusarium fujikuroi</i>	Catalytic activity
YP_0012493 08.1	-6.96	Cytochrome C oxidase subunit 2 (mitochondrion)	<i>Fusarium graminearum</i>	Energy metabolism
KPA41675.1	-5.98	DNA helicase INO80	<i>Fusarium langsethiae</i>	DNA helicase complex
KPA45353.1	-5.33	Transcription factor	<i>Fusarium langsethiae</i>	-
KPA42477.1	-5.07	DNA repair protein RAD18	<i>Fusarium langsethiae</i>	Cellular response to DNA damage stimulus
OAQ71859.1	-3.93	Helix-turn-helix domain-containing protein	<i>Purpureocillium lilacinum</i>	-
SCB64018.1	-3.87	Unnamed protein product	<i>Fusarium graminearum</i>	-
KPA46585.1	-3.41	Heat shock protein mitochondrial	<i>Fusarium langsethiae</i>	Mitochondrial part
KPA38919.1	-3.10	22kda glycoprotein	<i>Fusarium langsethiae</i>	-

1 FC represents Log₂(FONM/FON)

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1 Supplementary Table S4 Sequences of primers and predicted PCR product size

Protein Acc.	Sequence (5'-3')	Product size (bp)
KPA37403.1	F:GCCTGAACACCCTCCTCTAA R:TATGAAGAGAGTTGCGCCCA	133
KPA45232.1	F:TCTGTTCCCGCCATCTTC R:CCGCCTTCCGTGGTCTTA	107
KPA39795.1	F:AATGGCGGGTTGTTGGTT R:TCGCTTCAGTGCCTTTGC	86
CCT67575.1	F:CAGACTGGATGCCCTTGT R:TCTTCTACGGTTTCTACGAT	120
EXA53151.1	F: CTCATCAGGGTTGGGGAAGT R:TCCCTGGCACCAAGTATGTT	98
XP_964698.1	F:CCTGCGTAGAAGGTTGCATC R:GTGGTAAACGATCCGCTGAC	169
KIL86238.1	F:GAGCTACATCTTTCGCACGG R:GGACGACCGAAATGACAGTG	178
KPA44397.1	F:AAGATCCAGACCAGCGTTGA R:AGAACTCTACCTCCGTCCCT	217
EXA36265.1	F:ATCTCCAAGTCTGACGCCAA R:AACGTACAACCTGCGCAACTT	153

	F:CTCCAACGTCAACTTAGCCG	
KPA46791.1		104
	R:TTGTTTGAGCAGCGTCCATT	
	F:CTACCAAATTAGTGCGAGGGG	
YP_001249308.1		224
	R:GCTCACTTATCGGGCAAGC	
	F:TCTTCGAGGGGCTGACAATT	
EMT63775.1		178
	R:TGTGGAAGCCGTACCTGAAT	
1		
2		